



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jofuku, K. Diane
Okamuro, Jack K.

(ii) TITLE OF INVENTION: Methods for Improving Seeds

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/879,827
(B) FILING DATE: 20-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/700,152
(B) FILING DATE: 20-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Arg Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Trp Glu Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1680
- (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CTCTCTCTCT | CTCTTAGCT | CTTTTTTT | TTTGTTTC | ATTAAGTTT | TTATTTATT | 60 |
| TTCTACCAAC | CAAAAGCTT | TCTCTTGGT | TTCTCTTATT | TAGCTTCTAA | CCTTGAGGAG | 120 |
| AATATACCAAG | AGGATTGAAG | TTTGAACCTT | CAAAGATCAA | AATCAAGAAA | CCAAAAAA | 180 |
| ACAAAAAA | TGTGGGATCT | AAACGACGCA | CCACACCAA | CACAAAGAGA | AGAAGAATCT | 240 |
| GAAGAGTTT | GTTATTCTTC | ACCAAGTAAA | CGGGTTGGAT | CTTTCTCTAA | TTCAAGCTCT | 300 |
| TCAGCTGTTG | TTATCGAAGA | TGGATCCGAT | GACGATGAAC | TTAACCGGGT | CAGACCCAAT | 360 |

| | |
|--|------|
| AACCCACTTG TCACCCATCA GTTCTTCCT GAGATGGATT CTAACGGCGG TGGTGGCT | 420 |
| TCTGGCTTTC CTCGGGCTCA CTGGTTGGT GTTAAGTTT GTCAGTCGGA TCTAGCCACC | 480 |
| GGATCGTCCG CGGGTAAAGC TACCAACGTT GCCGCTGCCG TAGTGGAGCC GGCACAGCCG | 540 |
| TTGAAAAAGA GTCGGCGTGG ACCAAGATCA AGAAGTTCTC AGTATAGAGG TGTTACGTT | 600 |
| TACCGGCGTA CCGGAAGATG GGAATCTCAT ATTTGGGACT GTGGGAAACA AGTTTACTTA | 660 |
| GGTGGATTTG ACAC TGCGTCA CGAGCAGCT CGAGCATATG ATAGAGCTGC TATTAAATTC | 720 |
| CGTGGAGTAG AAGCGGATAT CAATTCAAC ATCGACGATT ATGATGATGA CTTGAAACAG | 780 |
| ATGACTAATT TAACCAAGGA AGAGTCGTA CACGTACTTC GCCGACAAAG CACAGGCTTC | 840 |
| CCTCGAGGAA GTTCGAAGTA TAGAGGTGTC ACTTGCATA AGTGTGGTC TTGGGAAGCT | 900 |
| CGTATGGGTC AATTCTTAGG CAAAAAGTAT GTTATTGG GTTTGTTCGA CACCGAGGTC | 960 |
| GAAGCTGCTA GAGCTTACGA TAAAGCTGCA ATCAAATGTA ACGGCAAAGA CGCCGTGACC | 1020 |
| AACTTGATC CGAGTATTAGG CGATGAGGAA CTCAATGCCG AGTCATCAGG GAATCCTACT | 1080 |
| ACTCCACAAG ATCACAAACCT CGATCTGAGC TTGGGAAATT CGGCTAATTG GAAGCATAAA | 1140 |
| AGTCAAGATA TGCGGCTCAG GATGAACCAA CAACAACAAG ATTCTCTCCA CTCTAATGAA | 1200 |
| GTTCTGGAT TAGGTCAAAC CGGAATGCTT AACCAACTC CCAATTCAAA CCACCAATT | 1260 |
| CCGGGCAGCA GCAACATTGG TAGCGGAGGC GGATTCTCAC TGTTCGGC GGCTGAGAAC | 1320 |
| CACCGGTTTG ATGGTCGGGC CTCGACGAAC CAAGTGTGA CAAATGCTGC AGCATCATCA | 1380 |
| GGATTCTCTC CTCATCATCA CAATCAGATT TTTAATTCTA CTTCTACTCC TCATCAAAAT | 1440 |
| TGGCTGCAGA CAAATGGCTT CCAACCTCCT CTCATGAGAC CTTCTGAAT CTTTTATATT | 1500 |
| TTTAAGGTTT ATTATTATAT AAGAAAAACA AAAATGAACC TTTGAAATCC CCACATGTT | 1560 |
| TTGGTCATTT CATTAATCAT CGGCTTATAT TTTGCTTATT TTCCCTAAAC TCCTCTTGT | 1620 |
| AACTTAGGCG AACAAAAAAA ATTAATGGAA ATCTTTTCC CTCCATCGGT TACAAAAATA | 1680 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at positions 129 to 195"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 32..49
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix (SEQ ID NO:6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30

Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45

Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
 50 55 60

Asp Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at positions 221 to 288"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..50
- (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix (SEQ ID NO:7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15

Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
 20 25 30

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 35 40 45

Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
 50 55 60
 Asp Glu Glu Leu
 65

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

U Phe Asp Thr Ala His Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile
 1 5 10 15

U Lys Phe

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 1 5 10 15

Lys Cys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala Tyr Asp
1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Cl
C1
Cn

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: /note= "ANT-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 44..59
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic alpha-helix (SEQ ID NO:37)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
1 5 10 15

Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg
20 25 30

Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala
35 40 45

Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr
50 55 60

His Thr Asn Phe Ser Ala Glu Asn Tyr Gln Lys Glu Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "ANT-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 37..51
- (D) OTHER INFORMATION: /note= "putative ANT-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
 1 5 10 15

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
 20 25 30

Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
 35 40 45

Ile Lys Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg
 50 55 60

Tyr Asp Val Asp Arg
 65

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "RAP2.7-R1 direct repeat"

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 33.49

(D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha helix (SEQ ID NO:3'6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
20 25 30

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45

Glu Asp Met
65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE 'CHARACTERISTICS':

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 26..34

(D) OTHER INFORMATION: /note= "putative RAP2.7-R2
amphipathic alpha-helix"

SEQUENCE DESCRIPTION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15

Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys Ala Ala
20 25 30

Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met Ser Ser
 35 40 45

Tyr Gln Asn Glu Ile
50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Arg Gly Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Trp Glu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Tyr Leu Gly
1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Ile Lys
1

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-1"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative EREBP-1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
1 5 10 15

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
20 25 30

Thr Tyr Glu Thr Asp Glu Glu Ala Ala Ile Ala Tyr Asp Lys Ala Ala
35 40 45

Tyr Arg Met Arg Gly Ser Lys Ala His Leu Asn Phe Pro Leu Glu Val
50 55 60

Ala Asn Phe Lys Gln
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-2"

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 35..51
 (D) OTHER INFORMATION: /note= "putative EREBP-2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

C1 | Gly Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
 1 5 10 15
 Cm | Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
 20 25 30
 Thr Tyr Glu Thr Ala Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala
 35 40 45
 Tyr Arg Met Arg Gly Ser Lys Ala Leu Leu Asn Phe Pro His Arg Ile
 50 55 60
 Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-3"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix (SEQ ID NO:41)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | |
|---|---|----|----|
| 1 | 5 | 10 | 15 |
|---|---|----|----|

| | | |
|----|----|----|
| 20 | 25 | 30 |
|----|----|----|

| | | |
|----|----|----|
| 35 | 40 | 45 |
|----|----|----|

| | | |
|----|----|----|
| 50 | 55 | 60 |
|----|----|----|

| | | | | |
|----|-----|-----|-----|-----|
| 65 | Asn | Gln | Ser | Pro |
|----|-----|-----|-----|-----|

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-4"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..51
- (D) OTHER INFORMATION: /note= "putative EREBP-4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | |
|---|---|----|----|
| 1 | 5 | 10 | 15 |
|---|---|----|----|

Ala Glu Ile Arg Asp Pro Asn Arg Lys Gly Thr Arg Val Trp Leu Gly
 20 25 30

Thr Phe Asp Thr Ala Ile Glu Ala Ala Lys Ala Tyr Asp Arg Ala Ala
 35 40 45

Phe Lys Leu Arg Gly Ser Lys Ala Ile Val Asn Phe Pro His Arg Ile
 50 55 60

Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.2 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix (SEQ ID NO:38)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg
 35 40 45

Arg Ile Arg Gly Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn
 50 55 60

Pro Ser Val Val
 65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.3 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..50
- (D) OTHER INFORMATION: /note= "putative RAP2.3 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Asn Val Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
 20 25 30

Phe Asn Thr Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys
 35 40 45

Gln Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His
 50 55 60

Pro Pro Pro Pro
 65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linéar

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.5 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix (SEQ ID NO:39)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Arg | Tyr | Arg | Gly | Val | Arg | Lys | Arg | Pro | Trp | Gly | Arg | Tyr | Ala |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 |
| Ala | Glu | Ile | Arg | Asp | Pro | Gly | Lys | Lys | Thr | Arg | Val | Trp | Leu | Gly | Thr |
| | | | | | | | 20 | | 25 | | | | | 30 | |
| Phe | Asp | Thr | Ala | Glu | Glu | Ala | Ala | Arg | Ala | Tyr | Asp | Thr | Ala | Ala | Arg |
| | | | | | | | 35 | | 40 | | | | | 45 | |
| Asp | Phe | Arg | Gly | Ala | Lys | Ala | Lys | Thr | Asn | Phe | Pro | Thr | Phe | Leu | Glu |
| | | | | | | | 50 | | 55 | | | | | 60 | |
| Leu | Ser | Asp | Gln | | | | | | | | | | | | |
| | | | | | | | 65 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.6 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.6 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Lys | Tyr | Arg | Gly | Val | Arg | Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala |
| 1 | | | | | | 5 | | | | 10 | | | | | 15 |
| Ala | Glu | Ile | Arg | Asp | Pro | His | Lys | Ala | Thr | Arg | Val | Trp | Leu | Gly | Thr |
| | | | | | | | 20 | | 25 | | | | | 30 | |
| Phe | Glu | Thr | Ala | Glu | Ala | Ala | Arg | Ala | Tyr | Asp | Ala | Ala | Leu | | |
| | | | | | | | 35 | | 40 | | | | | 45 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Arg | Gly | Ser | Lys | Ala | Lys | Leu | Asn | Phe | Pro | Glu | Asn | Val | Gly |
| 50 | | | | | 55 | | | | | 60 | | | | | |
| Thr | Gln | Thr | Ile | | | | | | | | | | | | |
| 65 | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.12 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic alpha-helix (SEQ ID NO:40)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Gln | Tyr | Arg | Gly | Ile | Arg | Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Ile | Arg | Asp | Pro | Arg | Glu | Gly | Ala | Arg | Ile | Trp | Leu | Gly | Thr |
| | | 20 | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Thr | Ala | Glu | Glu | Ala | Ala | Arg | Ala | Tyr | Asp | Ala | Ala | Arg |
| | 35 | | | | | 40 | | | | | | 45 | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Arg | Gly | Ser | Lys | Ala | Lys | Val | Asn | Phe | Pro | Glu | Asn | Met |
| | 50 | | | | 55 | | | | | 60 | | | | |

| | | | |
|-----|-----|-----|-----|
| Lys | Ala | Asn | Ser |
| 65 | | | |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis TINY AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative TINY amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Val | Tyr | Arg | Gly | Val | Arg | Lys | Arg | Asn | Trp | Gly | Lys | Trp | Val |
| 1 | | | | | 5 | | | | | | 10 | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Ile | Arg | Glu | Pro | Arg | Lys | Lys | Ser | Arg | Ile | Trp | Leu | Gly | Thr |
| | 20 | | | | | | 25 | | | | | | | | 30 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Ser | Pro | Glu | Met | Ala | Ala | Arg | Ala | His | Asp | Val | Ala | Ala | Leu |
| | | | | | 35 | | | 40 | | | | | | | 45 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Lys | Gly | Ala | Ser | Ala | Ile | Leu | Asn | Phe | Pro | Asp | Leu | Ala | Gly |
| | 50 | | | | | 55 | | | | | | | | | 60 |

| | | | |
|-----|-----|-----|-----|
| Ser | Phe | Pro | Arg |
| | 65 | | |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.1 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Pro | Tyr | Arg | Gly | Ile | Arg | Arg | Arg | Lys | Trp | Gly | Lys | Trp | Val |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 |

Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser
 20 25 30

Tyr Thr Thr Asp Ile Ala Ala Arg Ala Tyr Asp Val Ala Val Phe
 35 40 45

Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu
 50 55 60

Gln Glu Glu Asp
 65

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

C114

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.4 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val
 1 5 10 15

Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr
 35 40 45

Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asn Leu Arg His
 50 55 60

Asn Gly Phe His
 65

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.8 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..48
- (D) OTHER INFORMATION: /note= "putative RAP2.8 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly
 1 5 10 15

Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn
 20 25 30

Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe
 35 40 45

Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly
 50 55 60

Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.10 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative RAP2.10 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Pro | Tyr | Lys | Gly | Ile | Arg | Met | Arg | Lys | Trp | Gly | Lys | Trp | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Glu | Ile | Arg | Glu | Pro | Asn | Lys | Arg | Ser | Arg | Ile | Trp | Leu | Gly | Ser |
| | 20 | | | | | | 25 | | | | | | 30 | | |
| Tyr | Ser | Thr | Pro | Glu | Ala | Ala | Arg | Ala | Tyr | Asp | Thr | Ala | Val | Phe | |
| | | 35 | | | | | 40 | | | | | | 45 | | |
| Tyr | Leu | Arg | Gly | Pro | Ser | Ala | Arg | Leu | Asn | Phe | Pro | Glu | Leu | Leu | Ala |
| | | 50 | | | | | 55 | | | | | 60 | | | |
| Gly | Val | Thr | Val | | | | | | | | | | | | |
| | 65 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Chink
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.11 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..50
- (D) OTHER INFORMATION: /note= "putative RAP2.11 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Lys | Phe | Val | Gly | Val | Arg | Gln | Arg | Pro | Ser | Gly | Lys | Trp | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Glu | Ile | Lys | Asp | Thr | Thr | Gln | Lys | Ile | Arg | Met | Trp | Leu | Gly | Thr |
| | 20 | | | | | | 25 | | | | | | 30 | | |
| Phe | Glu | Thr | Ala | Glu | Glu | Ala | Ala | Arg | Ala | Tyr | Asp | Glu | Ala | Ala | Cys |
| | | 35 | | | | | | 40 | | | | | 45 | | |

Leu Leu Arg Gly Ser Asn Thr Arg Thr Asn Phe Ala Asn His Phe Pro
50 55 60
Asn Asn Ser Gln
65

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Val or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cat Tyr Arg Gly Xaa Arg
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = positively charged amino acid"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Trp, Phe or Tyr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Arg or Lys"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Asp or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Trp Gly Xaa Xaa Xaa Ala Glu Ile Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

Clut
 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ser or Thr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Leu Gly Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile, Leu or positively charged amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Glu Ala Ala Xaa Ala Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

U

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CK Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
 1 5 10 15
 Ile Arg

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
1 5 10 15

Ile Arg

(2) INFORMATION FOR SEQ ID NO:41:

Ch
✓

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg Glu Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "AP2 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys Gln Met Thr Asn Leu Thr Lys Glu Glu Phe Val His Val Leu Arg
1 5 10 15

Arg Gln Ser Thr Gly Phe Pro Arg Gly
20 25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

C

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "ANT linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Asp Met Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu
1 5 10 15

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
20 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "RAP2.7 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Lys Gln Val Gln Asn Leu Ser Lys Glu Glu Phe Val His Ile Leu
 1 5 10 15
 Arg Arg Gln Ser Thr Gly Phe Ser Arg Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = positively charged
 amino acid"

✓
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn Leu Thr Xaa Glu Glu Phe Val His
 1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Arg Arg Gln Ser Thr Gly Phe Ser Arg Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JOAP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGCCGCTG CCGTAGTG

18

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JOAP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGTTCATCCT GAGCCGCATA TC

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "JORAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAAGAAGA AGTGCCTAAC CACG

24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGAAGCTA GAAGAGCGTC GA

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAATGGG CTGCGGAG

18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTTACCTCCA GCATCGAACG AG

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTGGATCTT GTTTCGCTTA CG

22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTTCAAGCT TAGCGTCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGATGGGCTT GAAACCCGAC

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGGCTAGGG CTACGCGC

18

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCTTTGCCT CCTCAACCAT TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTGAGTTCC AACATTTTCG GG

22

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAAATTGGTA ACTCCGGTTC CG

22

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCATTTGCT TTGGCGCATT AC

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCGTTACGC CTCTACCGG

19

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCCGTCTTC CAGAACGTTC

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "JORAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATCACGGATC TGGCTTGGTT C

21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "JORAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCCTTCTTCC GTATCAACGT CG

22

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..19
 (D) OTHER INFORMATION: /note= "JORAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCAACTCCG GCGGTTACG

19

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCCTTATA TACGCCGCCG A

21

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAGAAGAGCA AAGGCAACAA GAC

23

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTTGTTAGG AAAATGGTTT GCG

23

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAACCATTG TTTCACTTC GACTC

25

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCACAGAGCG TTTCTGAGAA TTAGC

25

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "AP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGTGGGATC TAAACGACGC AC

22

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

C19
 (A) NAME/KEY: -
 (B) LOCATION: 1..19
 (D) OTHER INFORMATION: /note= "AP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCTTGGTC CACGCCGAC

19

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "RAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAGAGGACCA TCTCTCAG

18

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACACTCGCT AGCTTCTC

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGGTCAGCA GCCAACAC

18

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAATGCATAG AGCTTGAGG

19

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ACGGATTTCATCGGAG

18

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAAGCTAGA ATCGAATCC

19

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TACCGGTTTC GCGCGTAG

18

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:


 (A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "RAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CACCTTCGAA ATCAACGACC G

21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCCCCGAAA ATGTTGGAAC TC

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "RAP2.6L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGAGAGAA AAAATTGGTA GATCG

25

(2) INFORMATION FOR SEQ ID NO:83:

Cont

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGATGGAGAC GAAGACTC

18

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTCGGAACCG GAGTTACC

18

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCACTCAAAG GCCGAGATC

19

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TAACAAACATC ACCGGCTCG

19

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCTT AGGAGGAG

18

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

*Cly
W*

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGCCTCATAT GAGTCAGAG

19

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCCCGGAGCT TTTAGCCG

18

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAACCCGTTC CAACGATCC

19

(2) INFORMATION FOR SEQ ID NO:91:

U

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "RAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCTTCACCA GAAGCAGAGC ATG

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCCATTGAT TGCATATAGG GACG

24

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCTTTGGTTC AGAACTCGAA CATC

24

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGGTTGATAA ACGAACGATG CG

22

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Lys Lys Ser Arg
1

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCATGCCAC GATCAACC

18

(2) INFORMATION FOR SEQ ID NO:97:

C114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGCAGTCAA TGCGACGG

18

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Trp Ala Ala Glu Ile Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Ala Asp Ser
1

(2) INFORMATION FOR SEQ ID NO:100:

*C1
Cmt*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: /note= "RAP2.1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | |
|--|-----|
| GAAGAGTCTA CGATGAGAAA GAGAAGGCAG CCACCTCAAG AAGAAGTGCC TAACCACGTG | 60 |
| GCTACAAGGA AGCCGTACAG AGGGATACGG AGGAGGAAAGT GGGGCAAGTG GGTGGCTGAG | 120 |
| ATTCGTGAGC CTAACAAACG CTCACGGCTT TGGCTTGGCT CTTACACAAAC CGATATCGCC | 180 |
| GCCGCTAGAG CCTACGACGT GGCCGTCTTC TACCTCCGTG GCCCCTCCGC ACGTCTCAAC | 240 |
| TTCCCTGATC TTCTCTTGCA AGAAGAGGAC CATCTCTCAG CCGCCACCAC CGCTGACATG | 300 |
| CCCGCAGCTC TTATAAGGGA AAAAGCGCG GAGGTGGCG CCAGAGTCGA CGCTCTTCTA | 360 |
| GCTTCTGCCG CTCCTTCGAT GGCTCACTCC ACTCCGCCGG TAATAAAACC CGACTTGAAT | 420 |
| CAAATACCCG AATCCGGAGA TATATAGTCA ATTTATATAC ATGTAGTTG TTTTGTGTTGA | 480 |
| TTAGAAGATT ACATTTACAT ACAAGATACA CATAGATACT GGAAAATATA GGTATGTATA | 540 |
| CATTCATAAA TTATCTTATG TATCAAAGAA TTTTATAGAT TCTGATTAGC TTTTGTGTTT | 600 |

| | |
|--|-----|
| TGTTTTGAT AAGAACTCTG ATTAGTTGTC CGGAGACAAA ACCGGCTAAG AGCAATCCAT | 660 |
| GAGAAGCTAG CGAGTGTGTT TTAGTTCAAG TTGTAATATA AATGCATATT AATTCTTAG | 720 |
| TAATTTGT | 729 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1101
- (C) OTHER INFORMATION: /note= "RAP2.2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | |
|--|------|
| CGTCCTTGGG GAAAATGGGC TGCAGGAGATC CGTGATCCGA GAAAAGGCTC CCGAGAATGG | 60 |
| CTTGAAACAT TCGACACTGC TGAGGAAGCA GCAAGAGCTT ATGATGCTGC AGCACGCAGA | 120 |
| ATCCGTGGCA CGAAAGCTAA GGTGAATTT CCCGAGGAGA AGAACCCCTAG CGTCGTATCC | 180 |
| CAGAAACGTC CTAGTGCTAA GACTAATAAT CTTCAGAAAT CAGTGGCTAA ACCAAACAAA | 240 |
| AGCGTAACCT TGGTTCAGCA GCCAACACAT CTGAGTCAGC AGTACTGCAA CAACTCCTT | 300 |
| GACAACCTT TTGGTGATAT GAGTTTCATG GAAGAGAAGC CTCAGATGTA CAACAATCAG | 360 |
| TTTGGGTTAA CAAACTCGTT CGATGCTGGA GGTAAACAATG GATACCAGTA TTTCAGTTCC | 420 |
| GATCAGGGCA GTAACCCCTT CGACTGTTCT GAGTTGGGT GGAGTGATCA CGGCCCTAAA | 480 |
| ACACCCGAGA TCTCTCAAT GCTTGTCAAT AACAAACGAAG CATCATTGAT TGAAGAAACC | 540 |
| AATGCAGCCA AGAAGCTCAA ACCAAACTCT GATGAGTCAG ACGATCTGAT GGCATACCTT | 600 |
| GACAACGCCT TGTGGGACAC CCCACTAGAA GTGGAAGCCA TGCTTGGCGC AGATGCTGGT | 660 |
| GCTGTGACTC AGGAAGAGGA AAACCCAGTG GAGCTATGGA GCTTAGATGAT GATCAATTTC | 720 |
| ATGCTGGAAG GAGACTTTG AAGTGATCGA TGGTTCCCTTA GTTTGTAAAT AAAGCTGTGT | 780 |
| TGGATTTGC TGTTGGGGGA TGGTACAAGT CACACCTCAA GCTCTATGCA TTGGTATCTC | 840 |
| ATGAGCCTTC TCTTCCATAG AGAGTTCTC TTTAATTTT GTCGAAATAA AAAAGGTGTG | 900 |
| ATGAAGTAAA TAGAGGTATA ATAATATCTA TCTATTAAGT CTTGTTTGT TCTTCATT | 960 |
| TTGTATTTCT TTTCTATTTA AAAGACAGTT TATTAGTCTT CTGAGCTCTC TTTTGATCT | 1020 |
| TTGTTATAGC GTATCATCAC CCTCGAAAGT GTAATGTTT GTACCCCCAA ACTTGTAG | 1080 |

CATTATAATA AAGTCTCTTT G

1101

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1055
- (C) *W*
- (D) OTHER INFORMATION: /note= "RAP2.3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | | | | | | |
|------------|--------------|-------------|------------|------------|------------|------|
| ATAAAGGCAT | TTCAGCTCCA | CCGTAGGAAA | CTTTCTCTTG | AAAGAAACCC | ACAGCAACAA | 60 |
| ACAGAGAAAA | TGTGTGGCGG | TGCTATTATT | TCCGATTATG | CCCCTCTCGT | CACCAAGGCC | 120 |
| AAGGGCCGTA | AACTCACGGC | TGAGGAACTC | TGGTCAGAGC | TCGATGCTTC | CGCCGCCGAC | 180 |
| GACTTCTGGG | GTTTCTATTTC | CACCTCCAAA | CTCCATCCCA | CCAACCAAGT | TAACGTGAAA | 240 |
| GAGGAGGCAG | TGAAGAAGGA | GCAGGCAACA | GAGCCGGGGA | AACGGAGGAA | GAGGAAGAAT | 300 |
| GTTTATAGAG | GGATACGTAACG | GGCTCCATGG | GGAAAATGGG | CGGCTGAGAT | TCGAGATCCA | 360 |
| CGAAAAGGTG | TTAGAGTTTG | GCTTGGTACG | TTCAACACGG | CGGAGGAAGC | TGCCATGGCT | 420 |
| TATGATGTTG | CGGCCAAGCA | GATCCGTGGT | GATAAAGCCA | AGCTCAACTT | CCCAGATCTG | 480 |
| CACCATCCTC | CTCCTCCTAA | TTATACTCCT | CCGCCGTCA | CGCCACGATC | AACCGATCAG | 540 |
| CCTCCGGCGA | AGAAGGTCTG | CGTTGTCTCT | CAGAGTGAGA | GCGAGTTAAG | TCAGCCGAGT | 600 |
| TTCCCGGTGG | AGTGTATAGG | ATTTGGAAAT | GGGGACGAGT | TTCAGAACCT | GAGTTACGGA | 660 |
| TTTGAGCCGG | ATTATGATCT | GAAACAGCAG | ATATCGAGCT | TGGAATCGTT | CCTTGAGCTG | 720 |
| GACGGTAACA | CGGCGGAGCA | ACCGAGTCAG | CTTGATGAGT | CCGTTCCGA | GGTGGATATG | 780 |
| TGGATGCTTG | ATGATGTCAT | TGCGTCGTAT | GAGTAAAAGA | AAAAAAATAA | GTTTAAAAAA | 840 |
| AGTTAAATAA | AGTCTGTAAT | ATATATGTAAC | CCGCCGTTAC | TTTTAAAAGG | TTTTTACCGT | 900 |
| CGCATTGGAC | TGCTGATGAT | GTCTGTTGTG | TAATGTGTAG | AATGTGACCA | AATGGACGTT | 960 |
| ATATTACGGT | TTGTGGTATT | ATTAGTTCT | TAGATGGAAA | AACTTACATG | TGTAAATAAG | 1020 |
| ATTTGTAATG | TAAGACGAAG | TACTTATAAC | TTCTT | | | 1055 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

Cl
Wt

- (A) NAME/KEY: -
- (B) LOCATION: 1..969
- (D) OTHER INFORMATION: /note= "RAP2.4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|-------------|-----|
| TCTTCCTCCG | ACGCATCACA | ACAACAAACAA | CTCTTCTCG | AATCTTCTCA | GCCCAAAGCC | 60 |
| GTACTGATG | AAGCAATCTG | GAGTCGCTGG | ATCTTGTTC | GCTTACGGTT | CAGGTGTTCC | 120 |
| TTCGAAGCCG | ACGAAGCTTT | ACAGAGGTGT | GAGGCAACGT | CACTGGGGAA | AATGGGTGGC | 180 |
| TGAGATCCGT | TTGCCGAGAA | ATCGGACTCG | TCTCTGGCTT | GGGACTTTG | ACACGGCGGA | 240 |
| GGAAGCTGCG | TTGGCCTATG | ATAAGGCGGC | GTACAAGCTG | CGCGGCGATT | TCGCCCCGGCT | 300 |
| TAACCTCCCT | AACCTACGTC | ATAACGGATT | TCACATCGGA | GGCGATTCG | GTGAATATAA | 360 |
| ACCTCTTCAC | TCCTCAGTCG | ACGCTAACGT | TGAAGCTATT | TGTAAAAGCA | TGGCGGAGAC | 420 |
| TCAGAACACAG | GACAAATCGA | CGAAATCATC | GAAGAAACGT | GAGAAGAAGG | TTTCGTCGCC | 480 |
| AGATCTATCG | GAGAAAGTGA | AGGCAGGAGGA | GAATTGGTT | TCGATCGGTG | GATCTCCACC | 540 |
| GGTACGGAG | TTTGAAGAGT | CCACCGCTGG | ATCTTCGCCG | TTGTCGGACT | TGACGTTCCG | 600 |
| TGACCCGGAG | GAGCCGCCGC | AGTGGAACGA | GACGTTCTCG | TTGGAGAAAGT | ATCCGTCGTA | 660 |
| CGAGATCGAT | TGGGATTTCGA | TTCTAGCTTA | GGGGAAAAT | AGGAAATTCA | GCCGCTTGCA | 720 |
| ATGGAGTTTT | TGTGAAATTG | CATGACTGGC | CCAAGAGTAA | TTAATTAAAT | ATGGATTAGT | 780 |
| GTAAATTTC | GTATGTTAAT | ATTTGTATTA | TGGTTGTAT | TAGTCTCTCT | GTGTCGGTCC | 840 |
| AGCTTGCAGG | TTTTGTCAG | GCTCGACCAT | GCCACAGTTT | TCATTTATG | TAATCTTTT | 900 |
| TTCTTTGTC | TTATGTAATT | TGTAGCTTC | GTTCTTCAT | CTATAATGCA | ATTTTATTAT | 960 |
| GATTATGTG | | | | | | 969 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..937
- (C) OTHER INFORMATION: /note= "RAP2.5"

CJ
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| GTCGACCCAC GCGTCCGACT CTCTCTCTAA TCTATCTATC CGAGAATGGC CAAGATGGC | 60 |
| TTGAAACCCG ACCCGGCTAC TACTAACCAAG ACCCACATAA ATGCCAAGGA GATTGTTAC | 120 |
| AGAGGCGTTA GGAAGCGTCC TTGGGGCCGT TATGCCGCCG AGATCCGAGA TCCGGGCAAG | 180 |
| AAAACCCGCG TCTGGCTTGG CACTTCGAT ACGGCTGAAG AGGCGGCGCG TGCTTACGAT | 240 |
| ACGGCGGCCGC GTGATTTCG TGTTGCTAAG GCTAAGACCA ATTTCCAAC TTTTCTCGAG | 300 |
| CTGAGTGACC AGAAGGTCCC TACCGGTTTC GCGCGTAGCC CTAGCCAGAG CAGCACGCTC | 360 |
| GACTGTGCTT CTCCTCCGAC GTTAGTTGTG CCTTCAGCGA CGGCTGGAA TGTTCCCCCG | 420 |
| CAGCTCGAGC TTAGTCTCGG CGGAGGAGGC GGCGGCTCGT GTTATCAGAT CCCGATGTCG | 480 |
| CGTCCTGTCT ACTTTTGGA CCTGATGGGG ATCGGTAACG TAGGTCGTGG TCAGCCTCCT | 540 |
| CCTGTGACAT CGGCGTTAG ATGCCGGTG GTGCATGTTG CGACGAAGAT GGCTTGTGGT | 600 |
| GCCCAAAGCG ACTCTGATTC GTCATCGTC GTTGATTCG AAGGTGGAT GGAGAAGAGA | 660 |
| TCTCAGACTG TTAGATCTAG ATCTTAATTT GCCTCCTCCA TCGGAACAGG CCTGAGCTTT | 720 |
| TAACGGTGTC GTTTCAATTC GAAGCGCATG CGTTTCTTCT TCTTTTGAG CTGTGAAAAT | 780 |
| TCGTTTCTC ATAGTTTTC CTCTCTCTCT CTCTCAGTCT AAATTATTA CCAGTTTTA | 840 |
| GAAAGAAAAA ACAGATTAAA TCTGAGAGAG AAAAATATAA TTTAGCTGA CATGGATCGT | 900 |
| TATGTACATA TTATTACATA ACCGGAGATC TGAACGT | 937 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..651
- (C) OTHER INFORMATION: /note= "RAP2.6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AAGAGAAGAG | TTTCCTTGC | CTCCTCAACC | ATTGATTACC | GGTCAGCTG | TGACTAAAGA | 60 |
| ATGTGAAAGC | TCAATGTCCT | TGGAGAGGCC | AAAAAAATAT | AGAGGAGTAA | GGCAACGACC | 120 |
| ATGGGGAAAA | TGGCGGCCGG | AGATTCGAGA | CCCACACAAG | GCGACACGTG | TATGGCTTGG | 180 |
| GACATTCGAG | ACAGCCGAGG | CCGCCGCAAG | AGCCTATGAT | CGGGCAGCAC | TTCGCTTAG | 240 |
| AGGAAGCAAA | GCAAAGCTTA | ATTCCTCGA | AAATGTTGGA | ACTCAGACGA | TTCAACGAAA | 300 |
| TTCTCATTTC | TTGCAAAACT | CAATGCAACC | TTCTCTAAC | TACATCGATC | AATGTCCAAC | 360 |
| TCTATTATCT | TACTCTCGAT | GTATGGAGCA | ACAACAACCA | TTAGTAGGCA | TGTTGCAGCC | 420 |
| AACAGAAGAG | GAAAATCACT | TTTCGAAAAA | ACCATGGACC | GAATATGATC | AATACAATT | 480 |
| CTCCTCTTT | GGTTAACTAA | CATATCGTCA | ACGCTTGT | TTTCTACTTA | TTCGATCTAC | 540 |
| CAATTTTTC | TCTCCCAATA | CAACTTCAGT | CTGATTATTG | CCTTCTTAGA | TATGTCTTCG | 600 |
| AATGTTATGA | CTATACATGG | GTGTATATAA | AATTGTGAT | CAAAGTCTTG | T | 651 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(1)
WT

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1329
- (D) OTHER INFORMATION: /note= "RAP2.7"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AATGCCGATG | GAGACGAAGA | CTCTTGCTCT | ACTCGAGCTT | TCACTCTCAG | TTTCGATATT | 60 |
| TTAAAAGTCG | GAAGTAGTAG | CGGCAGAGAC | GAAAGCCCCG | CCGCTTCAGC | TTCCGTTACT | 120 |
| AAAGAGTTTT | TTCCGGTGAG | TGGAGACTGT | GGACATCTAC | GAGATGTTGA | AGGATCATCA | 180 |
| AGCTCTAGAA | ACTGGATAGA | TCTTCTTTT | GACCGTATTG | GTGACGGAGA | AACGAAATTG | 240 |
| GTAACCTCGG | TTCCGACTCC | GGCTCCGGTT | CCGGCTCAGG | TTAAAAAGAG | TCGGAGAGGA | 300 |
| CCAAGGTCTA | GAAGTTCAC | GTATAGAGGA | GTACTTTTT | ATAGAAGAAC | TGGTCGATGG | 360 |
| GAGTCACATA | TTGGGGATTG | TGGGAAACAA | GTTTATTTAG | GTGGTTTCGA | CACTGCTCAT | 420 |
| GCTGCAGCTA | GAGCTTATGA | TCGAGCTGCT | ATTAATTTA | GAGGTGTTGA | TGCTGATATC | 480 |
| AACTTTACTC | TTGGTGATTA | TGAGGAAGAT | ATGAAACAGG | TACAAAAC | GAGTAAGGAA | 540 |

| | |
|---|------|
| GAGTTTGTGC ATATACTGCG TAGACAGAGC ACGGGGTTT CGCGGGGAG TTCGAAGTAT | 600 |
| CGAGGGGTTA CGTTACACAA ATGTGGTAGA TGGGAAGCTA GGATGGGCA GTTTCTTGGT | 660 |
| AAAAAGGCTT ATGACAAGGC TGCAATCAAC ACTAATGGTA GAGAAGCAGT CACGAACCTC | 720 |
| GAGATGAGTT CATAACCAAAA TGAGATTAAC TCTGAGAGCA ATAACCTCTGA GATTGACCTC | 780 |
| AACTTGGGAA TCTCTTATC GACCGGTAAT GCGCCAAAGC AAAATGGGAG GCTCTTCAC | 840 |
| TTCCCTTCTA ATACTTATGA AACTCAGCGT GGAGTTAGCT TGAGGATAGA TAACGAATAC | 900 |
| ATGGGAAAGC CGGTGAATAC ACCTCTTCCT TATGGATCCT CGGATCATCG CCTTTACTGG | 960 |
| AACGGAGCAT GCCCGAGTTA TAATAATCCC GCCGAGGGAA GAGCAACAGA AAAGAGAAGT | 1020 |
| GAAGCTGAAG GGATGATGAG TAACTGGGAA TGGCAGAGAC CGGGGCAAAC AAGGCCGTG | 1080 |
| AGACCGCAGC CACCGGGACC ACAACCACCA CCATTGTTCT CAGTTGCAGC AGCATCATCA | 1140 |
| GGATTCTCAC ATTTCCGGCC ACAACCTCCC AATGACAATG CAACACGTGG TTACTTTAT | 1200 |
| CCACACCCCTT AACTGTAAAG GGGACATATG AGAGTTTTT TACCATCTCT CTCTCTCTCA | 1260 |
| ACACTCTAGT CCCCTTCAA AAATGTCATT TGGGTTTAG ATTTTCACA TACAATGATC | 1320 |
| AATTTTTCC | 1329 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

01/07

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1113
- (D) OTHER INFORMATION: /note= "RAP2.8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|-----|
| CGCCACCACC GCCAAGAAC TCTCTCCTCC TCCCGCGGCG GCGTTACGCC TCTACCGGAT | 60 |
| GGGAAGCGGC GGGAGCAGCG TCGTGTGGA TCCCGAGAAC GGCCTAGAGA CGGAGTCACG | 120 |
| AAAGCTACCA TCTTCAAAAT ACAAAAGGTGT TGTTCTCAG CCTAACGGAA GATGGGGAGC | 180 |
| TCAGATCTAC GAGAACGACC AACGAGTATG GCTCGGGACT TTCAACGAGC AAGAAGAAC | 240 |
| TGCTCGTTCC TACGACATCG CAGCTTGTAG ATTCCGTGGC CGCGACGCCG TCGTCAACTT | 300 |
| CAAGAACGTT CTGGAAGACG GCGATTAGC TTTTCTTGAA GCTCACTCAA AGGCCGAGAT | 360 |
| CGTCGACATG TTGAGAAAAC ACACCTACGC CGACGAGCTT GAACAGAAC AATAAACGGCA | 420 |

| | |
|--|------|
| GTTGTTTCTC TCCGTCGACG CTAACGGAAA ACGTAACGGA TCGAGTACTA CTCAAAACGA | 480 |
| CAAAGTTTA AAGACGTGTG AAGTTCTTT CGAGAAGGCT GTTACACCTA GCGACGTTGG | 540 |
| GAAGCTAAAC CGTCTCGTGA TACCTAAACA ACACGCCGAG AAACACTTTC CGTTACCGTC | 600 |
| ACCGTCACCG GCAGTGACTA AAGGAGTTT GATCAACTTC GAAGACGTTA ACGGTAAAGT | 660 |
| GTGGAGGTTG CGTTACTCAT ACTGGAACAG TAGTCAAAGT TACGTGTTGA CCAAGGGATG | 720 |
| GAGTCGATTG GTCAAGGAGA AGAATCTCG AGCCGGTGAT GTTGTACTT TCGAGAGATC | 780 |
| GACCGGACTA GAGCGGCAGT TATATATTGA TTGGAAAGTT CGGTCTGGTC CGAGAGAAAA | 840 |
| CCCGGTTCAAG GTGGTGGTTC GGCTTTCCGG AGTTGATATC TTTAATGTGA CCACCGTGAA | 900 |
| GCCAAACGAC GTCGTGGCCG TTTGCGGTGG AAAGAGATCT CGAGATGTTG ATGATATGTT | 960 |
| TGCGTTACGG TGTTCCAAGA AGCAGGCGAT AATCAATGCT TTGTGACATA TTTCCTTTTC | 1020 |
| CGATTTATG CTTTCGTTT TTAATTTTT TTTTGTCAA GTTGTGAGG TTGTGATTCA | 1080 |
| TGCTAGGTTG TATTTAGGAA AAGAGATAAG ACC | 1113 |

(2) INFORMATION FOR SEQ ID NO:108:

C/Int

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..417
- (D) OTHER INFORMATION: /note= "RAP2.9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|---|-----|
| CGATCACCGGA TCTGGCTTGG TTCATACAAA ACCGCCGTTG CCGCGGCACG GGCCTACGAT | 60 |
| ACCGCTGTGT TTTACTTACG TGGTCCTTCG GCGAGACTCA ATTTCCCTGA AGAGGTCTTT | 120 |
| AAGGATGGAA ACGGCGGTGA AGGCTTAGGA GGAGATATGT CTCCGACGTT GATACTGGAAAG | 180 |
| AAGGC GGCTG AGGTGGGAGC TAGAGTCGAC GCAGAGTTGC GGTTAGAGAA TAGGATGGTT | 240 |
| GAGAACTTAG ACATGAATAA GTTGCCGGAG GCATATGGAT TGTAATTAT AGTTGGTAG | 300 |
| TTTATAGGTT GGAGATTGCC CGGAGACAGA GTCAAACAGA GGTTCTCTGA CTCATATGAG | 360 |
| GCATAATATA GTTAATATAG TAATTTTGT TTTGAGCATA GTAATTATGT CATAACC | 417 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..814
- (C) OTHER INFORMATION: /note= "RAP2.10"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| ATTTTTTGAA | ACTTCTTCTC | TTTGCGGTT | TCGTGTTCCA | CTCCTCTCTT | CTTGGCCCAC | 60 |
| GTGTTCATCA | ATCTCTCCCT | CCGCATGTAA | TCGCTTCGCC | GTCAATATCA | CATCTTCTT | 120 |
| CTTCTTTATC | TTTAAAATCT | CTTTAGATCG | ATTCTTTGT | GGATTCTTGA | AATCTCCGGA | 180 |
| GAAAACCACT | ATGGAGACGG | CGACTGAAGT | GGCACCGGTG | GTGTCAACTC | CGGCGGTTAC | 240 |
| GGTTGCGGCG | GTGGCGACGA | GGAAGAGAGA | TAAGCCGTAT | AAAGGGATAA | GGATGAGGAA | 300 |
| GTGGGGGAAG | TGGGTGGCGG | AGATAAGAGA | GCCTAATAAA | AGGTCAAGGA | TCTGGCTTGG | 360 |
| CTCTTACTCT | ACTCCTGAAG | CGGCGGCGCG | TGCTTACGAC | ACGGCGGTGT | TTTATCTCCG | 420 |
| AGGTCTTCT | GCTCGGCTTA | ACTTCCCGGA | GCTTTAGCC | GGAGTGACGG | TGACGGGAGG | 480 |
| AGGCGGAGGA | GGAGTGAAACG | GTGGTGGAGA | TATGTCGGCG | GCGTATATAA | GGAGAAAAGC | 540 |
| GGCGGAGGTT | GGAGCACAAG | TGGATGCGTT | AGAAGCGGCG | GGGGCGGGAG | GGAATCGTCA | 600 |
| TCATCATCAT | CATCAACATC | AACGTGGTAA | TCATGATTAC | GTAGATAATC | ATAGTGATT | 660 |
| TCGTATTAAT | GATGATCTTA | TGGAGTGTAG | TAGTAAAGAA | GGGTTTAAGA | GGTGTAAATGG | 720 |
| ATCGTTGGAA | CGGGTTGATT | TAAACAAATT | ACCCGATCCG | GAAACTTCAG | ATGACGATTA | 780 |
| GGAAAGCAAA | AAATAGAAAC | AAAAAAAAAA | AAAA | | | 814 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..933
- (D) OTHER INFORMATION: /note= "RAP2.11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|--|-----|
| AAAAAAATAT GGAACATCAA ACAACTCAA AGCAGAAAAC TAAGGAGAAG AGCAAAGGCA | 60 |
| ACAAGACTAA ^D GTTTGTGGGA GTTAGGCAAA GGCCTTCAGG AAAATGGGTG GCAGAGATCA | 120 |
| AAGACACTAC ACAAAAGATA CGGATGTGGC TCGGAACCTT TGAAACCGCA GAAGAAGCCG | 180 |
| CTCGAGCCTA CGATGAAGCT GCATGTCTCT TACGTGGCTC CAATACTCGC ACCAATTCG | 240 |
| CAAACCATT TCCTAACAAAC TCACAACAT CTTTGAAGAT CAGAAATCTT CTTCACCAGA | 300 |
| AGCAGAGCAT GAAGCAGCAG CAACAACAAAC AACACAAACC AGTTTCTTCT TTAACGGATT | 360 |
| GCAACATCAA CTACATCTCG ACTGCTACTA GTCTCACCAC AACCACCACC ACCACCACTA | 420 |
| CCACGGCCAT ACCGCTCAAT AATGTGTACC GACCAGATTC ATCGGTCTT CGGCAACCAG | 480 |
| AAACCGAGGG TCTCCAGCTT CCTTATTCTG GGCCCCTTGT CTCTGGATTCA ACCATCAGA | 540 |
| TTCCATTGGC TCAGGCAGGG GGAGAAACAC ATGGACATCT CAACGATCAC TACTCAACCG | 600 |
| ATCAACATTG GGGTCTTGCA GAAATTGAAA GACAGATATC TGCGTCCCTA TATGCAATGA | 660 |
| ATGGAGCTAA CAGTTACTAT GACAACATGA ATGCAGAATA TGCAATTTC GATCCTACCG | 720 |
| ATCCCATTG GGATCTCCCT TCACTCTCCC AACTCTTCTG CCCTACGTGA TTTCCAATT | 780 |
| ACTTTCTG ATCAATTCTAT GTAATGTTTG GATCAATGAT CCATGATTGT AAAGTAGAAC | 840 |
| ACATCTCTAC AATGTTCCAA TAGACAAGAT TGTACCTAAA GAAAATGGAC AATGTAAGAA | 900 |
| GATAATGAAG GTTTCGTACA ACAAAAGCTT GAT | 933 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1277
- (D) OTHER INFORMATION: /note= "RAP2.12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|---|----|
| CGTTCGAATT TCTTCGATTT TGACGCTGAG TTCGAAGCTG ATTTCCAAGG TTTCAAAGAT | 60 |
|---|----|

| | |
|--|------|
| GATTCGTCTA TCGATTGCGA TGATGATTTC GACGTCGGTG ATGTTTCGC CGATGTGAAA | 120 |
| CCATTCGTTT TCACCTCGAC TCCAAAACCC GCCGTCTCCG CCGCTGCGGA AGGTCAGTT | 180 |
| TTTGGTAAGA AAGTTACTGG CTTGGATGGG GACGCTGAGA AATCTGCAAA TAGGAAGAGG | 240 |
| AAGAATCAGT ACCGAGGGAT TAGGCAACGT CCTTGGGGAA AATGGGCTGC TGAGATAACGT | 300 |
| GATCCAAGGG AAGGTGCTAG AATCTGGCTT GGAACGTTCA AGACAGCTGA GGAAGCTGCT | 360 |
| AGAGCTTACG ATGCTGCAGC GCGGAGAATC CGTGGATCTA AAGCTAAGGT GAATTTCCCT | 420 |
| GAAGAAAACA TGAAGGCTAA TTCTCAGAAA CGCTCTGTGA AGGCTAATCT TCAGAAACCA | 480 |
| GTGGCTAAAC CTAACCCTAA CCCAAGTCCA GCTTGGTTC AGAACTCGAA CATCTCCTT | 540 |
| GAAAATATGT GTTTCATGGA GGAGAACAC CAAGTGAGCA ACAACAACAA CAACCAGTT | 600 |
| GGGATGACAA ACTCCGTTGA TGCTGGATGT AATGGGTATC AGTATTTCAG CTCTGACCAG | 660 |
| GGTAGTAATT CTTTCGATTG TTGGAGTTT GGTTGGAGCG ATCAAGCTCC GATAACTCCC | 720 |
| GACATCTCTT CTGCGGTTAT CAACAACAAC AACTCAGCTC TGTTCTTGA GGAAGCCAAT | 780 |
| CCAGCTAAGA AGCTCAAGTC TATGGATTTC GAGACACCTT ACAACAACAC TGAATGGGAC | 840 |
| GCTTCACTGG ATTTCCTCAA CGAAGATGCT GTAACGACTC AGGACAATGG TGCAAACCC | 900 |
| ATGGACCTAT GGAGTATTGA TGAAATTCAAT TCCATGATTG GAGGAGTCTT CTGAAGAGAT | 960 |
| CCAGTTTCAT GTAAATAAGG CTGCATGTTT GTGAGTTCC CGCATCGTTC GTTTATCAAC | 1020 |
| CTCCAAAACT TTCTAATGTC TGTTACTTGC ATCTTCTTCT GCTGTCTCTG TCTGTCTCTC | 1080 |
| TCAGGAGTTC CTGTTGCAT TGCAGAGAAGC CATGAGCCTC TATCTGAGG GTAGTTGTGA | 1140 |
| TGAAGTTAAG TAGAGGCTTA TTTTAGGGG TTGTGGTAGT TTTTGTTTA GTGAATCTT | 1200 |
| TGAATTGTT TGTGTTTGT TTTGTTACT TTATGCCCA AAACCTCTT AACATTTGTC | 1260 |
| ATAATGTGTT TGAACCT | 1277 |

C
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